

SEQUENCE LISTING

<110> Maliszewski, Charles R.
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Immunex Corporation
Cornell Research Foundation, Inc.

<120> Methods of Inhibiting Platelet Activation and Recruitment

<130> 23,495 USA

<140> US 09/807,660
<141> 2001-09-06

<150> US 60/104,585
<151> 1998-10-16

<150> US 60/107,466
<151> 1998-11-06

<150> US 60/149,010
<151> 1999-08-13

<160> 37

<170> PatentIn version 3.1

<210> 1
<211> 1599
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (67)..(1596)

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ccacaccaag cagcggctgg gggggggaaa gacgaggaaaa gaggagggaaa acaaaagctg 60

ctactt atg gaa gat aca aag gag tct aac gtg aag aca ttt tgc tcc 108
Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser
1 5 10

aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156
Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
15 20 25 30

gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204
Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
50 55 60

tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 300
Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
65 70 75

cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 348
His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
80 85 90

gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 396
Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
95 100 105 110

aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt	Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val	444	
115	120	125	
tac ctg gga gcc acg gca ggc atg cggttgcctcaggatggaaagt gaa	Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu	492	
130	135	140	
gag ttg gca gac agg gtt ctg gat gtgttgatggaggatgcctcagcaac	Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn	540	
145	150	155	
tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa	Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu	588	
160	165	170	
ggt gcc tat ggc tgg att act atc aac tat ctgttgatggc aaa ttc agt	Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser	636	
175	180	185	190
cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag	Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln	684	
195	200	205	
gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act	Glu Thr Phe Gly Ala Leu Asp Leu Gly Ala Ser Thr Gln Val Thr	732	
210	215	220	
ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa	Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln	780	
225	230	235	
ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg	Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu	828	
240	245	250	
tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att	Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile	876	
255	260	265	270
cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga	Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly	924	
275	280	285	
tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc	Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr	972	
290	295	300	
aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt	Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly	1020	
305	310	315	
att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac	Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn	1068	
320	325	330	
acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg	Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu	1116	
335	340	345	350
cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg	Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val	1164	
355	360	365	
atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg	Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val	1212	
370	375	380	
act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa		1260	

Thr	Glu	Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	
385							390					395				
aca	tct	tac	gct	gga	gta	aag	gag	aag	tac	ctg	agt	gaa	taa	tgc	ttt	1308
Thr	Ser	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	
400					405					410						
tct	ggg	acc	tac	att	ctc	tcc	ctc	ctt	ctg	caa	ggt	tat	cat	ttc	aca	1356
Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr		
415					420				425					430		
gct	gat	tcc	tgg	gag	cac	atc	cat	ttc	att	ggc	aag	atc	cag	ggc	agc	1404
Ala	Asp	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	
									440					445		
gac	gcc	ggc	tgg	act	ttg	ggc	tac	atg	ctg	aac	ctg	acc	aac	atg	atc	1452
Asp	Ala	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	
									455					460		
cca	gct	gag	caa	cca	ttg	tcc	aca	cct	ctc	tcc	cac	tcc	acc	tat	gtc	1500
Pro	Ala	Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr	Tyr	Val	
									470					475		
ttc	ctc	atg	gtt	cta	ttc	tcc	ctg	gtc	ctt	ttc	aca	gtg	gcc	atc	ata	1548
Phe	Leu	Met	Val	Leu	Phe	Ser	Leu	Val	Leu	Phe	Thr	Val	Ala	Ile	Ile	
								485				490				
ggc	ttg	ctt	atc	ttt	cac	aag	cct	tca	tat	ttc	tgg	aaa	gat	atg	gta	1596
Gly	Leu	Leu	Ile	Phe	His	Lys	Pro	Ser	Tyr	Phe	Trp	Lys	Asp	Met	Val	
						495				505					510	
tag																1599

<210> 2
 <211> 510
 <212> PRT
 <213> Homo sapiens

<400> 2																
Met	Glu	Asp	Thr	Lys	Glu	Ser	Asn	Val	Lys	Thr	Phe	Cys	Ser	Lys	Asn	
1					5				10					15		
Ile	Leu	Ala	Ile	Leu	Gly	Phe	Ser	Ser	Ile	Ile	Ala	val	Ile	Ala	Leu	
									20			25		30		
Leu	Ala	Val	Gly	Leu	Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn	Val	Lys	
									35			40		45		
Tyr	Gly	Ile	val	Leu	Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile	
									50			55		60		
Tyr	Lys	Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln	
									65			70		75		80
Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln	
									85			90		95		
Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	
									100			105		110		
Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	
									115			120		125		
Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	
									130			135		140		
Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	
									145			150		155		160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
 165 170 175
 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
 180 185 190
 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
 195 200 205
 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
 210 215 220
 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
 225 230 235 240
 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
 245 250 255
 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
 260 265 270
 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
 275 280 285
 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
 290 295 300
 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
 305 310 315 320
 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
 325 330 335
 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
 340 345 350
 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
 355 360 365
 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
 370 375 380
 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
 385 390 395 400
 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
 405 410 415
 Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
 420 425 430
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
 435 440 445
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
 450 455 460
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
 465 470 475 480
 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
 485 490 495
 Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
 500 505 510

<211> 476
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 3
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15
Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30
Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
35 40 45
Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
50 55 60
Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65 70 75 80
Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
85 90 95
Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
100 105 110
Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
115 120 125
Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
130 135 140
Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
145 150 155 160
Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
165 170 175
Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
180 185 190
Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195 200 205
Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
210 215 220
Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225 230 235 240
Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
245 250 255
Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
260 265 270
Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
275 280 285
Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
290 295 300
Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
325 330 335
Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
340 345 350
Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
355 360 365
Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380
Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400
Tyr Ala Gly val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415
Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
420 425 430
Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
435 440 445
Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
450 455 460
Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470 475

<210> 4
<211> 476
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<220>
<221> VARIANT
<222> (39)
<223> Any amino acid, preferably Cys or Ser

<400> 4
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Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30
Ile Phe Leu Ser Ser Met Xaa Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45
Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
50 55 60
Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65 70 75 80
Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
85 90 95
Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
100 105 110
Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
 130 135 140
 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
 145 150 155 160
 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
 165 170 175
 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
 180 185 190
 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
 195 200 205
 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
 210 215 220
 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
 225 230 235 240
 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
 245 250 255
 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
 260 265 270
 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
 275 280 285
 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
 290 295 300
 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
 305 310 315 320
 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
 325 330 335
 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
 340 345 350
 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
 355 360 365
 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
 370 375 380
 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
 385 390 395 400
 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
 405 410 415
 Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
 420 425 430
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
 435 440 445
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
 450 455 460
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470 475

<210> 5
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<220>
<221> CDS
<222> (1)..(1362)

<400> 5
gca cct act tca agt tct aca aag aaa aca cag cta act agt tca acc 48
Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
1 5 10 15

cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg gat 96
Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30

gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca gaa 144
Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
35 40 45

aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg gtt 192
Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
50 55 60

aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata ggc 240
Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
65 70 75 80

att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca agg 288
Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg
85 90 95

tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc atg 336
Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
100 105 110

cg^g ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg gat 384
Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
115 120 125

gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt gcc 432
Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
130 135 140

agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act atc 480
Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
145 150 155 160

aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc ata 528
Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile
165 170 175

gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac ctt 576
Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu
180 185 190

ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act atc 624
Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile
195 200 205

gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac tac 672
Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr
210 215 220

aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca ctc	720
Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu	
225 230 235 240	
tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att ctc	768
Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu	
245 250 255	
agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta agt	816
Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser	
260 265 270	
gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt cca	864
Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro	
275 280 285	
ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc cat	912
Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His	
290 295 300	
caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc cag	960
Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln	
305 310 315 320	
tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt ggg	1008
Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly	
325 330 335	
gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca tca	1056
Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser	
340 345 350	
gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc tgt	1104
Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys	
355 360 365	
gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag gag	1152
Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu	
370 375 380	
aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc ctc	1200
Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu	
385 390 395 400	
ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc cat	1248
Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His	
405 410 415	
ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc tac	1296
Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr	
420 425 430	
atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc aca	1344
Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr	
435 440 445	
cct ctc tcc cac tcc acc taa	1365
Pro Leu Ser His Ser Thr	
450	

<210> 6
<211> 454

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion

construct of human CD39

<400> 6
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
1 5 10 15
Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30
Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
35 40 45
Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
50 55 60
Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
65 70 75 80
Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg
85 90 95
Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
100 105 110
Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
115 120 125
Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
130 135 140
Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
145 150 155 160
Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile
165 170 175
Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu
180 185 190
Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile
195 200 205
Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr
210 215 220
Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu
225 230 235 240
Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu
245 250 255
Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser
260 265 270
Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro
275 280 285
Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His
290 295 300
Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln
305 310 315 320
Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly
325 330 335
Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser
340 345 350

Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys
 355 360 365
 Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu
 370 375 380
 Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu
 385 390 395 400
 Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His
 405 410 415
 Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr
 420 425 430
 Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr
 435 440 445
 Pro Leu Ser His Ser Thr
 450

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<210> 7
<211> 1437
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<220>
<221> CDS
<222> (1)..(1434)

tac	ctg	gga	gcc	acg	gca	ggc	atg	cgg	ttg	ctc	agg	atg	gaa	agt	gaa	432
Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	
130					135					140						
gag	ttg	gca	gac	agg	gtt	ctg	gat	gtg	gtg	gag	agg	agc	ctc	agc	aac	480
Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	
145					150					155					160	
tac	ccc	ttt	gac	ttc	cag	ggt	gcc	agg	atc	att	act	ggc	caa	gag	gaa	528
Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	
									165	170						
ggt	gcc	tat	ggc	tgg	att	act	atc	aat	tat	ctg	ctg	ggc	aaa	ttc	agt	576
Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	
								180	185							
cag	aaa	aca	agg	tgg	ttc	agc	ata	gtc	cca	tat	gaa	acc	aat	aat	cag	624
Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	
							195	200			205					
gaa	acc	ttt	gga	gct	ttg	gac	ctt	ggg	gga	gcc	tct	aca	caa	gtc	act	672
Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	
						210	215			220						
ttt	gta	ccc	caa	aac	cag	act	atc	gag	tcc	cca	gat	aat	gct	ctg	caa	720
Phe	Val	Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	
						225	230			235					240	
ttt	cgc	ctc	tat	ggc	aag	gac	tac	aat	gtc	tac	aca	cat	agc	ttc	ttg	768
Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	
						245	250			255						
tgc	tat	ggg	aag	gat	cag	gca	ctc	tgg	cag	aaa	ctg	gcc	aag	gac	att	816
Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	
						260	265			270						
cag	gtt	gca	agt	aat	gaa	att	ctc	agg	gac	cca	tgc	ttt	cat	cct	gga	864
Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	
						275	280			285						
tat	aag	aag	gta	gtg	aac	gta	agt	gac	ctt	tac	aag	acc	ccc	tgc	acc	912
Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	
						290	295			300						
aag	aga	ttt	gag	atg	act	ctt	cca	ttc	cag	cag	ttt	gaa	atc	cag	ggt	960
Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	
						305	310			315					320	
att	gga	aac	tat	caa	caa	tgc	cat	caa	agc	atc	ctg	gag	ctc	ttc	aac	1008
Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	
						325	330			335						
acc	agt	tac	tgc	cct	tac	tcc	cag	tgt	gcc	ttc	aat	ggg	att	ttc	ttg	1056
Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	
						340	345			350						
cca	cca	ctc	cag	ggg	gat	ttt	ggg	gca	ttt	tca	gct	ttt	tac	ttt	gtg	1104
Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	
						355	360			365						
atg	aag	ttt	tta	aac	ttg	aca	tca	gag	aaa	gtc	tct	cag	gaa	aag	gtg	1152
Met	Lys	Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	
						370	375			380						
act	gag	atg	atg	aaa	aag	ttc	tgt	gct	cag	cct	tgg	gag	gag	ata	aaa	1200
Thr	Glu	Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	
						385	390			395					400	
aca	tct	tac	gct	gga	gta	aag	gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	1248

Thr	Ser	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe
				405					410					415	
tct	ggc	acc	tac	att	ctc	tcc	ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca
Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr
				420				425					430		
gct	gat	tcc	tgg	gag	cac	atc	cat	ttc	att	ggc	aag	atc	cag	ggc	agc
Ala	Asp	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser
				435				440				445			
gac	gcc	ggc	tgg	act	ttg	ggc	tac	atg	ctg	aac	ctg	acc	aac	atg	atc
Asp	Ala	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile
				450				455			460				
cca	gct	gag	caa	cca	ttg	tcc	aca	cct	ctc	tcc	cac	tcc	acc	taa	
Pro	Ala	Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr		
				465				470			475				

<210> 8

<211> 478

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 8

Met	Ala	Leu	Trp	Ile	Asp	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu
1				5					10					15	

Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys
				20				25					30		

Lys	Thr	Gln	Leu	Thr	Ser	Ser	Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn
		35						40				45			

Val	Lys	Tyr	Gly	Ile	Val	Leu	Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu
	50				55					60					

Tyr	Ile	Tyr	Lys	Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val
	65				70				75				80		

His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe
		85						90					95		

Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu
		100						105					110		

Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val
	115				120						125				

Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu
	130				135					140					

Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn
	145				150					155				160	

Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu
					165				170				175		

Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser
					180				185				190		

Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln
							195			200			205		

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
 210 215 220
 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
 225 230 235 240
 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
 245 250 255
 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
 260 265 270
 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
 275 280 285
 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
 290 295 300
 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
 305 310 315 320
 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
 325 330 335
 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
 340 345 350
 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
 355 360 365
 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
 370 375 380
 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
 385 390 395 400
 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
 405 410 415
 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
 420 425 430
 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
 435 440 445
 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
 450 455 460
 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470 475

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
signal sequence

<400> 9

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser
 20

<210> 10
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 10
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 11
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 11
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys
35 40

<210> 12
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 12
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys
20 25

<210> 13
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 13
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys
20 25 30

<210> 14
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 14
ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60
tgtccacacc tctctccac gagcccc 87

<210> 15
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 15
gatcggggct cgtgggagag aggtgtggac aatggttgct cagctggat catgttggtc 60
aggtaaaaaa tgttagccaa agtccag 87

<210> 16
<211> 740
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (42)..(737)

<400> 16
cggtaaccgt agcgtcgaca ggcctaggat atcgatacgt a gag ccc aga tct tgt 56
Glu Pro Arg Ser Cys
1 5

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag ggc 104
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
10 15 20

gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 152
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
25 30 35

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 200
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
40 45 50

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 248
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
55 60 65

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac 296
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
70 75 80 85

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 344
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
90 95 100

aag gac tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atg 392
16

Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Met	
105						110										115
cag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	440
Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
120						125									130	
tac	acc	ctg	ccc	cca	tcc	cg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	488
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
135						140					145					
ctg	acc	tgc	ctg	gtc	aaa	g	tc	ta	cc	agg	cac	atc	gcc	gtg	gag	536
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg	His	Ile	Ala	Val	Glu	
150					155					160					165	
tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	584
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
	170				175						180					
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	632
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	
	185				190						195					
gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	680
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	
	200				205					210						
cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	728
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
	215				220					225						
ccg	ggt	aaa	tga													740
Pro	Gly	Lys														
230																

<210> 17
<211> 232
<212> PRT
<213> Homo sapiens

<400> 17																
Glu	Pro	Arg	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	
1				5				10						15		
Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Pro	Lys	Pro
	20				25									30		
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	
	35				40									45		
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	
	50				55									60		
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	
	65				70					75					80	
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	
	85				90										95	
Asp	Trp	Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	
	100				105									110		
Leu	Pro	Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	
	115				120									125		
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	
	130				135						140					

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
145 150 155 160

His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 18
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 18
ctttccatcc tgagcaac 18

<210> 19
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 19
aaaaaaacttag tcagaacaaa gcttgccag aaaacg 36

<210> 20
<211> 24
<212> PRT
<213> Mus sp.

<400> 20

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
1 5 10 15

Leu Val Leu Leu Pro Val Thr Ser
20

<210> 21
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 21
 ctatgttctgg agactacaaa gatgacgatg acaaaaccca gaacaa 46

<210> 22
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 22
 agctttgttc tgggtttgt catcgcatc tttgttagtct ccagaa 46

<210> 23
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 23
 ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60
 tgtccacacc tctctccac tccacctaa 89

<210> 24
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24
 ggccttaggt ggagtggag agaggtgtgg acaatggttg ctcagctggg atcatgttgg 60
 tcaggttcag catgtagccc aaagtccag 89

<210> 25
 <211> 1464
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1461)

<220>
 <223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 25
 atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta 48
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa	144
Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Asp Lys	
35 40 45	
acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg	192
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu	
50 55 60	
gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca	240
Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala	
65 70 75 80	
gaa aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg	288
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg	
85 90 95	
gtt aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata	336
Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile	
100 105 110	
ggc att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca	384
Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro	
115 120 125	
agg tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc	432
Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly	
130 135 140	
atg cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg	480
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu	
145 150 155 160	
gat gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt	528
Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly	
165 170 175	
gcc agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act	576
Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr	
180 185 190	
atc aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc	624
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser	
195 200 205	
ata gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac	672
Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp	
210 215 220	
ctt ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act	720
Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr	
225 230 235 240	
atc gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac	768
Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp	
245 250 255	
tac aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca	816
Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala	
260 265 270	
ctc tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att	864
Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile	
275 280 285	
ctc agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta	912
Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val	
290 295 300	
agt gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt	960

Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg	Phe	Glu	Met	Thr	Leu	
305					310				315						320	
cca	tcc	cag	cag	ttt	gaa	atc	cag	ggt	att	gga	aac	tat	caa	caa	tgc	1008
Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys	
									330						335	
cat	caa	agc	atc	ctg	gag	ctc	ttc	aac	acc	agt	tac	tgc	cct	tac	tcc	1056
His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	
									345						350	
cag	tgt	gcc	ttc	aat	ggg	att	ttc	ttg	cca	cca	ctc	cag	ggg	gat	ttt	1104
Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	Leu	Gln	Gly	Asp	Phe	
								360				365				
ggg	gca	ttt	tca	gct	ttt	tac	ttt	gtg	atg	aag	ttt	tta	aac	ttg	aca	1152
Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys	Phe	Leu	Asn	Leu	Thr	
								375			380					
tca	gag	aaa	gtc	tct	cag	gaa	aag	gtg	act	gag	atg	atg	aaa	aag	ttc	1200
Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu	Met	Met	Lys	Lys	Phe	
								390		395					400	
tgt	gct	cag	cct	tgg	gag	gag	ata	aaa	aca	tct	tac	gct	gga	gta	aag	1248
Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser	Tyr	Ala	Gly	Val	Lys	
								405		410			415			
gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	tct	ggt	acc	tac	att	ctc	tcc	1296
Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly	Thr	Tyr	Ile	Leu	Ser	
								420		425			430			
ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	gct	gat	tcc	tgg	gag	cac	atc	1344
Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp	Ser	Trp	Glu	His	Ile	
							435		440			445				
cat	ttc	att	ggc	aag	atc	cag	ggc	agc	gac	gcc	ggc	tgg	act	ttg	ggc	1392
His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala	Gly	Trp	Thr	Leu	Gly	
							450		455			460				
tac	atg	ctg	aac	ctg	acc	aac	atg	atc	cca	gct	gag	caa	cca	ttg	tcc	1440
Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	Pro	Ala	Glu	Gln	Pro	Leu	Ser	
							465		470		475			480		
aca	cct	ctc	tcc	cac	tcc	acc	taa									1464
Thr	Pro	Leu	Ser	His	Ser	Thr										
							485									

<210> 26

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 26

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
20 25 30

Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys
35 40 45

Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
50 55 60

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
 65 70 75 80
 Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
 85 90 95
 Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
 100 105 110
 Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
 115 120 125
 Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
 130 135 140
 Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
 145 150 155 160
 Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
 165 170 175
 Ala Arg Ile Ile Thr Gly Gln Glu Gly Ala Tyr Gly Trp Ile Thr
 180 185 190
 Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser
 195 200 205
 Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
 210 215 220
 Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr
 225 230 235 240
 Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp
 245 250 255
 Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala
 260 265 270
 Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile
 275 280 285
 Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val
 290 295 300
 Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
 305 310 315 320
 Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys
 325 330 335
 His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser
 340 345 350
 Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe
 355 360 365
 Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr
 370 375 380
 Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe
 385 390 395 400
 Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys
 405 410 415
 Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser
 420 425 430

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile
435 440 445

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly
450 455 460

Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
465 470 475 480

Thr Pro Leu Ser His Ser Thr
485

<210> 27

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 27

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys Ala Leu Pro
20 25 30

Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr
35 40 45

Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly
50 55 60

Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser
65 70 75 80

Lys Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys
85 90 95

Met Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr
100 105 110

Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu
115 120 125

Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu
130 135 140

Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln
145 150 155 160

Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys
165 170 175

Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn
180 185 190

Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln
195 200 205

Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala
210 215 220

Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser
225 230 235 240

Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys
 245 250 255
 Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His
 260 265 270
 Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro
 275 280 285
 Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile
 290 295 300
 Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu
 305 310 315 320
 Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile
 325 330 335
 Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr
 340 345 350
 Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu
 355 360 365
 Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu
 370 375 380
 Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr
 385 390 395 400
 Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His
 405 410 415
 Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln
 420 425 430
 Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn
 435 440 445
 Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 450 455 460

<210> 28
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 28
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15
 Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Thr Lys Lys Thr Gln Leu
 20 25 30
 Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
 35 40 45
 Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
 50 55 60

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
 65 70 75 80
 Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
 85 90 95
 Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu
 100 105 110
 Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
 115 120 125
 Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp
 130 135 140
 Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
 145 150 155 160
 Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
 165 170 175
 Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg
 180 185 190
 Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly
 195 200 205
 Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln
 210 215 220
 Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr
 225 230 235 240
 Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys
 245 250 255
 Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser
 260 265 270
 Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val
 275 280 285
 Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu
 290 295 300
 Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr
 305 310 315 320
 Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys
 325 330 335
 Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln
 340 345 350
 Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu
 355 360 365
 Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met
 370 375 380
 Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala
 385 390 395 400
 Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr
 405 410 415
 Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp
 420 425 430

Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp
435 440 445

Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln
450 455 460

Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470

<210> 29

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 29

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr
20 25 30

Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile
35 40 45

Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp
50 55 60

Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu
65 70 75 80

Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn
85 90 95

Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val
100 105 110

Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr
115 120 125

Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg
130 135 140

Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe
145 150 155 160

Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp
165 170 175

Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp
180 185 190

Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala
195 200 205

Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn
210 215 220

Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly
225 230 235 240

Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp
245 250 255

Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn
 260 265 270
 Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val
 275 280 285
 Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met
 290 295 300
 Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln
 305 310 315 320
 Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro
 325 330 335
 Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly
 340 345 350
 Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn
 355 360 365
 Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys
 370 375 380
 Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly
 385 390 395 400
 Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile
 405 410 415
 Leu Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu
 420 425 430
 His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr
 435 440 445
 Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro
 450 455 460
 Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470

<210> 30
 <211> 463
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 30
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Ala Pro Thr Ser Thr Gln Asn Lys Ala Leu Pro Glu
 20 25 30
 Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
 35 40 45
 Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
 50 55 60
 Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
 65 70 75 80

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
450 455 460

<210> 31
<211> 58
<212> PRT
<213> Homo sapiens

<400> 31
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15
Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
50 55

<210> 32
<211> 11
<212> PRT
<213> artificial

<220>
<223> linker sequence

<400> 32

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 33
<211> 13
<212> PRT
<213> artificial

<220>
<223> linker sequence

<400> 33

Gly Ala Gly Gly Ala Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 34
<211> 10
<212> PRT
<213> artificial

<220>
<223> linker sequence

<400> 34

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 35
<211> 9
<212> PRT
<213> artificial

<220>
<223> linker sequence

<400> 35

Gly Thr Pro Gly Thr Pro Gly Thr Pro
1 5

<210> 36
<211> 26
<212> PRT
<213> artificial

<220>
<223> linker sequence

<400> 36

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 37
<211> 4
<212> PRT
<213> artificial

<220>
<223> linker sequence

<400> 37

Thr Ser Ser Gly
1